

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: ASHIKARI, Toshihiko  
TANAKA, Yoshikazu  
FUJIWARA, Hiroyuki  
NAKAO, Masahiro  
FUKUI, Yuko  
SAKAKIBARA, Keiko  
MIZUTANI, Masako  
KUSUMI, Takaaki
- (ii) TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ACYL  
GROUP TRANSFER ACTIVITY
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
  - (B) STREET: 1737 King Street, Suite 500
  - (C) CITY: Alexandria
  - (D) STATE: Virginia
  - (E) COUNTRY: United States
  - (F) ZIP: 22314-2756
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/894,356
  - (B) FILING DATE: 18-AUG-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: JP 7-67159
  - (B) FILING DATE: 17-FEB-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: JP 7-196915
  - (B) FILING DATE: 29-JUN-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: JP 8-46534
  - (B) FILING DATE: 30-JAN-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO PCT/JP96/00348
  - (B) FILING DATE: 16-FEB-1996
- (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Meuth, Donna M.  
(B) REGISTRATION NUMBER: 36,607  
(C) REFERENCE/DOCKET NUMBER: 001560-308

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 836-6620  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1703 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gentiana triflora* var. *japonica*  
(F) TISSUE TYPE: petal

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library  
(B) CLONE: pGAT4

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 6..1412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCATT ATG GAG CAA ATC CAA ATG GTG AAG GTT CTT GAA AAA TGC CAA	47
Met Glu Gln Ile Gln Met Val Lys Val Leu Glu Lys Cys Gln	
1 5 10	
GTT ACA CCA CCA TCT GAC ACA ACA GAT GTC GAG TTA TCG CTA CCG GTA	95
Val Thr Pro Pro Ser Asp Thr Thr Asp Val Glu Leu Ser Leu Pro Val	
15 20 25 30	
ACA TTC TTC GAT ATC CCC TGG TTG CAC TTG AAT AAG ATG CAG TCC CTT	143
Thr Phe Phe Asp Ile Pro Trp Leu His Leu Asn Lys Met Gln Ser Leu	
35 40 45	
CTG TTT TAC GAC TTT CCG TAC CCA AGA ACA CAT TTC TTG GAC ACT GTT	191
Leu Phe Tyr Asp Phe Pro Tyr Pro Arg Thr His Phe Leu Asp Thr Val	
50 55 60	

ATC	CCT	AAT	CTT	AAG	GCC	TCT	TTG	TCT	CTC	ACT	CTA	AAA	CAC	TAC	GTT	239
Ile	Pro	Asn	Leu	Lys	Ala	Ser	Leu	Ser	Leu	Thr	Leu	Lys	His	Tyr	Val	
	65						70					75				
CCG	CTT	AGC	GGA	AAT	TTG	TTG	ATG	CCG	ATC	AAA	TCG	GGC	GAA	ATG	CCG	287
Pro	Leu	Ser	Gly	Asn	Leu	Leu	Met	Pro	Ile	Lys	Ser	Gly	Glu	Met	Pro	
	80					85					90					
AAG	TTT	CAG	TAC	TCC	CGT	GAT	GAG	GGC	GAC	TCG	ATA	ACT	TTG	ATC	GTT	335
Lys	Phe	Gln	Tyr	Ser	Arg	Asp	Glu	Gly	Asp	Ser	Ile	Thr	Leu	Ile	Val	
95					100					105					110	
GCG	GAG	TCT	GAC	CAG	GAT	TTT	GAC	TAC	CTT	AAA	GGT	CAT	CAA	CTG	GTA	383
Ala	Glu	Ser	Asp	Gln	Asp	Phe	Asp	Tyr	Leu	Lys	Gly	His	Gln	Leu	Val	
				115					120					125		
GAT	TCC	AAT	GAT	TTG	CAT	GGC	CTT	TTT	TAT	GTT	ATG	CCA	CGG	GTT	ATA	431
Asp	Ser	Asn	Asp	Leu	His	Gly	Leu	Phe	Tyr	Val	Met	Pro	Arg	Val	Ile	
			130					135					140			
AGG	ACC	ATG	CAA	GAC	TAT	AAA	GTG	ATC	CCG	CTC	GTA	GCC	GTG	CAA	GTA	479
Arg	Thr	Met	Gln	Asp	Tyr	Lys	Val	Ile	Pro	Leu	Val	Ala	Val	Gln	Val	
		145					150					155				
ACC	GTT	TTT	CCT	AAC	CGT	GGC	ATA	GCC	GTG	GCT	CTG	ACG	GCA	CAT	CAT	527
Thr	Val	Phe	Pro	Asn	Arg	Gly	Ile	Ala	Val	Ala	Leu	Thr	Ala	His	His	
	160					165					170					
TCA	ATT	GCA	GAT	GCT	AAA	AGT	TTT	GTA	ATG	TTC	ATC	AAT	GCT	TGG	GCC	575
Ser	Ile	Ala	Asp	Ala	Lys	Ser	Phe	Val	Met	Phe	Ile	Asn	Ala	Trp	Ala	
175					180					185					190	
TAT	ATT	AAC	AAA	TTT	GGG	AAA	GAC	GCG	GAC	TTG	TTG	TCC	GCG	AAT	CTT	623
Tyr	Ile	Asn	Lys	Phe	Gly	Lys	Asp	Ala	Asp	Leu	Leu	Ser	Ala	Asn	Leu	
				195				200						205		
CTT	CCA	TCT	TTC	GAT	AGA	TCG	ATA	ATC	AAA	GAT	CTG	TAT	GGC	CTA	GAG	671
Leu	Pro	Ser	Phe	Asp	Arg	Ser	Ile	Ile	Lys	Asp	Leu	Tyr	Gly	Leu	Glu	
			210					215					220			
GAA	ACA	TTT	TGG	AAC	GAA	ATG	CAA	GAT	GTT	CTT	GAA	ATG	TTC	TCT	AGA	719
Glu	Thr	Phe	Trp	Asn	Glu	Met	Gln	Asp	Val	Leu	Glu	Met	Phe	Ser	Arg	
		225					230					235				
TTT	GGA	AGC	AAA	CCC	CCT	CGA	TTC	AAC	AAG	GTA	CGA	GCT	ACA	TAT	GTC	767
Phe	Gly	Ser	Lys	Pro	Pro	Arg	Phe	Asn	Lys	Val	Arg	Ala	Thr	Tyr	Val	
	240					245					250					
CTC	TCC	CTT	GCT	GAA	ATC	CAG	AAG	CTA	AAG	AAC	AAA	GTA	CTG	AAT	CTC	815
Leu	Ser	Leu	Ala	Glu	Ile	Gln	Lys	Leu	Lys	Asn	Lys	Val	Leu	Asn	Leu	
255					260					265					270	
AGA	GGA	TCC	GAA	CCG	ACA	ATA	CGT	GTA	ACG	ACG	TTC	ACA	ATG	ACG	TGT	863
Arg	Gly	Ser	Glu	Pro	Thr	Ile	Arg	Val	Thr	Thr	Phe	Thr	Met	Thr	Cys	
				275					280					285		

GGA TAC GTA TGG ACA TGC ATG GTC AAA TCA AAA GAT GAC GTC GTA TCA Gly Tyr Val Trp Thr Cys Met Val Lys Ser Lys Asp Asp Val Val Ser 290 295 300	911
GAG GAA TCA TCG AAC GAC GAA AAT GAG CTC GAG TAC TTC AGT TTT ACA Glu Glu Ser Ser Asn Asp Glu Asn Glu Leu Glu Tyr Phe Ser Phe Thr 305 310 315	959
GCG GAT TGC CGA GGA CTT CTG ACG CCC CCG TGT CCG CCT AAC TAC TTT Ala Asp Cys Arg Gly Leu Leu Thr Pro Pro Cys Pro Pro Asn Tyr Phe 320 325 330	1007
GGC AAC TGT CTT GCG TCA TGC GTT GCA AAA GCA ACA CAT AAA GAG TTA Gly Asn Cys Leu Ala Ser Cys Val Ala Lys Ala Thr His Lys Glu Leu 335 340 345 350	1055
GTT GGG GAT AAA GGG CTT CTT GTT GCA GTT GCA GCT ATT GGA GAA GCC Val Gly Asp Lys Gly Leu Leu Val Ala Val Ala Ala Ile Gly Glu Ala 355 360 365	1103
ATT GAA AAG AGG TTG CAC AAC GAA AAA GGC GTT CTT GCA GAT GCA AAA Ile Glu Lys Arg Leu His Asn Glu Lys Gly Val Leu Ala Asp Ala Lys 370 375 380	1151
ACT TGG TTA TCG GAA TCT AAT GGA ATC CCT TCA AAA AGA TTT CTC GGG Thr Trp Leu Ser Glu Ser Asn Gly Ile Pro Ser Lys Arg Phe Leu Gly 385 390 395	1199
ATT ACC GGA TCG CCT AAG TTC GAT TCG TAT GGT GTA GAT TTT GGA TGG Ile Thr Gly Ser Pro Lys Phe Asp Ser Tyr Gly Val Asp Phe Gly Trp 400 405 410	1247
GGA AAG CCT GCA AAA TTT GAC ATT ACC TCT GTT GAT TAT GCA GAA TTG Gly Lys Pro Ala Lys Phe Asp Ile Thr Ser Val Asp Tyr Ala Glu Leu 415 420 425 430	1295
ATT TAT GTG ATT CAG TCC AGG GAT TTT GAA AAA GGT GTG GAG ATT GGA Ile Tyr Val Ile Gln Ser Arg Asp Phe Glu Lys Gly Val Glu Ile Gly 435 440 445	1343
GTA TCA TTG CCT AAG ATT CAT ATG GAT GCA TTT GCA AAA ATC TTT GAA Val Ser Leu Pro Lys Ile His Met Asp Ala Phe Ala Lys Ile Phe Glu 450 455 460	1391
GAA GGC TTT TGC TCT TTG TCA TAGTCTCTTT AATAGAACCA TATTTGCTGC Glu Gly Phe Cys Ser Leu Ser 465	1442
AATAAAGTAC CAAGTCCTTT AGTAACACTA CACCAAACCC TACTTTCGAG GCGGGAACAC	1502
CACAACGAGG TTCAATCACT AGAAGGTTGT ACTTCATAAA TTCCAGAGGT CGAATATACA	1562
CCGTTGTCCT CTGAAAAGTT GAACCTCACA CCTGACATGG TGTTACGATA GGTATTGTAT	1622
AATGCCATTA TATACTTCCA TAAAGTATCC TATGCAATAG AGAACATGTT ATGTGTTAA	1682

AAAAAAAAAA AAAAAAAAAA A

1703

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1622 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Gentiana triflora* va. *japonica*
  - (F) TISSUE TYPE: petal
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA library
  - (B) CLONE: pGAT106
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 35..1471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAACCATTGA ATCCAATTAA TCTGATTTAT TAAG ATG GCA GGA AAT TCC GAG	52
Met Ala Gly Asn Ser Glu	
1 5	
GAT ATC AAA GTT CTT GAG AAA TGC CGT GTT GCG CCA CCA CCG GAC GCC	100
Asp Ile Lys Val Leu Glu Lys Cys Arg Val Ala Pro Pro Pro Asp Ala	
10 15 20	
GTC GCC GAG TTT ACA GTC CCA CTG TCG TTT TTC GAC ATG CGA TGG TTG	148
Val Ala Glu Phe Thr Val Pro Leu Ser Phe Phe Asp Met Arg Trp Leu	
25 30 35	
ATC TCT GAT GCA GAA CAC CAT CTG CAT TTC TAC AGA TTC CGC CAT CCT	196
Ile Ser Asp Ala Glu His His Leu His Phe Tyr Arg Phe Arg His Pro	
40 45 50	
TGT CCC AAC TCT AAA TTT ATC ATT TCA TCC ATT AAA TCG TCC CTT TCC	244
Cys Pro Asn Ser Lys Phe Ile Ile Ser Ser Ile Lys Ser Ser Leu Ser	
55 60 65 70	
CTT GTT CTC AAA CAC TTT CTT CCG TTA GCC GGG AAT TTG ATT TGG CCG	292
Leu Val Leu Lys His Phe Leu Pro Leu Ala Gly Asn Leu Ile Trp Pro	
75 80 85	

GTA	GAT	TCC	TCC	GAT	AGA	ATG	CCG	GAG	TTG	CGT	TAC	AAG	AAA	GGG	GAC	340
Val	Asp	Ser	Ser	Asp	Arg	Met	Pro	Glu	Leu	Arg	Tyr	Lys	Lys	Gly	Asp	
			90					95					100			
TCC	GTT	TCT	TTA	ACA	ATT	GCA	GAA	TCG	AGC	ATG	GAT	TTT	GAT	TAT	CTC	388
Ser	Val	Ser	Leu	Thr	Ile	Ala	Glu	Ser	Ser	Met	Asp	Phe	Asp	Tyr	Leu	
		105					110				115					
GCC	GGA	GAT	CAT	CAG	AGG	GAT	TCT	TAT	AAA	TTC	AAC	GAT	TTG	ATT	CCG	436
Ala	Gly	Asp	His	Gln	Arg	Asp	Ser	Tyr	Lys	Phe	Asn	Asp	Leu	Ile	Pro	
	120					125				130						
CAG	CTG	CCA	GAA	CCG	ATT	GTA	ACC	TCC	GGC	GAC	GAA	GTA	TTA	CCA	CTT	484
Gln	Leu	Pro	Glu	Pro	Ile	Val	Thr	Ser	Gly	Asp	Glu	Val	Leu	Pro	Leu	
135					140				145						150	
TTT	GCT	TTA	CAG	GTG	ACG	GTG	TTC	TCC	AAC	ACC	GGT	ATA	TGC	ATT	GGA	532
Phe	Ala	Leu	Gln	Val	Thr	Val	Phe	Ser	Asn	Thr	Gly	Ile	Cys	Ile	Gly	
			155					160					165			
CGC	AAT	CTT	CAT	CAA	GTT	CTT	GGT	GAT	GCC	AGT	TCT	TTT	CTG	CAT	TTT	580
Arg	Asn	Leu	His	Gln	Val	Leu	Gly	Asp	Ala	Ser	Ser	Phe	Leu	His	Phe	
			170					175					180			
AAT	AAA	TTA	TGG	GTT	TTG	GTT	GAC	AAA	TCC	AAT	GGA	GAT	TCA	TTA	AAG	628
Asn	Lys	Leu	Trp	Val	Leu	Val	Asp	Lys	Ser	Asn	Gly	Asp	Ser	Leu	Lys	
		185					190				195					
TTC	CTT	CCA	CTT	TCT	TCT	CTA	CCT	ATG	TAC	GAC	AGA	TCT	GTG	GTG	CAA	676
Phe	Leu	Pro	Leu	Ser	Ser	Leu	Pro	Met	Tyr	Asp	Arg	Ser	Val	Val	Gln	
	200					205				210						
GAT	CCA	TTT	CAT	ATT	CGT	CGA	AAA	ATC	TAC	AAT	GAA	AGA	AAA	CTG	CTC	724
Asp	Pro	Phe	His	Ile	Arg	Arg	Lys	Ile	Tyr	Asn	Glu	Arg	Lys	Leu	Leu	
215					220				225					230		
AAA	TCT	CAG	GGC	ACA	CCT	ACT	GTT	CTA	AAT	CCA	GCA	ATT	TCT	AAA	GAT	772
Lys	Ser	Gln	Gly	Thr	Pro	Thr	Val	Leu	Asn	Pro	Ala	Ile	Ser	Lys	Asp	
			235					240					245			
GAA	GTT	CGA	GCC	ACC	TTC	ATC	CTA	CAC	CCT	ATT	GAT	ATC	ATG	AAG	CTC	820
Glu	Val	Arg	Ala	Thr	Phe	Ile	Leu	His	Pro	Ile	Asp	Ile	Met	Lys	Leu	
			250					255					260			
AAG	AAA	TTC	ATT	TCG	TCA	AAA	AAT	CGC	AAC	TTA	ACC	GGT	AGT	AGT	AAT	868
Lys	Lys	Phe	Ile	Ser	Ser	Lys	Asn	Arg	Asn	Leu	Thr	Gly	Ser	Ser	Asn	
		265					270					275				
TAT	AAT	CTG	TCA	ACT	TTC	ACG	GTG	ACA	TCT	GCA	CTG	ATC	TGG	ACA	TGC	916
Tyr	Asn	Leu	Ser	Thr	Phe	Thr	Val	Thr	Ser	Ala	Leu	Ile	Trp	Thr	Cys	
	280					285					290					
TTG	TCG	AAA	TCA	TTA	GAC	ACC	GTC	GTA	AGA	GAG	AAG	GTG	GAA	GAG	GAT	964
Leu	Ser	Lys	Ser	Leu	Asp	Thr	Val	Val	Arg	Glu	Lys	Val	Glu	Glu	Asp	
295					300					305					310	

AAA CAT GCA GCA AAC TTA TGT GCT TTC ATC AAC TGC CGA CAA CGT TTT	1012
Lys His Ala Ala Asn Leu Cys Ala Phe Ile Asn Cys Arg Gln Arg Phe	
315 320 325	
GCT CCG CCG ATA CCT CAA AAT TAC TTT GGA AAT TGC ATA GTG CCT TGT	1060
Ala Pro Pro Ile Pro Gln Asn Tyr Phe Gly Asn Cys Ile Val Pro Cys	
330 335 340	
ATG GTG GGA TCG ACT CAT GAG CAA CTT GTA GGA AAT GAA GGG TTG TCG	1108
Met Val Gly Ser Thr His Glu Gln Leu Val Gly Asn Glu Gly Leu Ser	
345 350 355	
GTA GCT GCA ACC GCC ATC GGA GAT GCT ATC CAT AAG AGG TTA CAT GAC	1156
Val Ala Ala Thr Ala Ile Gly Asp Ala Ile His Lys Arg Leu His Asp	
360 365 370	
TAC GAA GGA ATT CTG AGA GGA GAT TGG ATA TCG CCG CCC CGA TCA ACA	1204
Tyr Glu Gly Ile Leu Arg Gly Asp Trp Ile Ser Pro Pro Arg Ser Thr	
375 380 385 390	
TCT GCG GCA CCA AGG TCG ACG CTC ATT TAT GTC GTT GGA TCC GCA CAA	1252
Ser Ala Ala Pro Arg Ser Thr Leu Ile Tyr Val Val Gly Ser Ala Gln	
395 400 405	
CGC AAT GTG CAT GAT TTT GAT GCA GAT TTT GGT TGG GGA AAG CTT GAA	1300
Arg Asn Val His Asp Phe Asp Ala Asp Phe Gly Trp Gly Lys Leu Glu	
410 415 420	
AAG CAT GAA TCT GTT TCA ACT AAT CCT TCG GCA ACA CTA ATT TTG ATC	1348
Lys His Glu Ser Val Ser Thr Asn Pro Ser Ala Thr Leu Ile Leu Ile	
425 430 435	
TCT CGG TCC AGA AGA TTT AAA GGA GCA CTT GAG CTT GGC ATT TCT TTG	1396
Ser Arg Ser Arg Arg Phe Lys Gly Ala Leu Glu Leu Gly Ile Ser Leu	
440 445 450	
CCT AAG AAT AGG ATG GAC GCA TTT GCC ACC ATT TTT ACG AAT TTC ATC	1444
Pro Lys Asn Arg Met Asp Ala Phe Ala Thr Ile Phe Thr Asn Phe Ile	
455 460 465 470	
AAT AGT CTC CAT GTG AGG AGC CCT TTG TAAGAAAAAA GTGGTATCAA	1491
Asn Ser Leu His Val Arg Ser Pro Leu	
475	
TGTATAAAAA AGACAGACAA GTTATGATGC AACAAATGTT TTAGGAGATT ACAAATCCAT	1551
GGGAAGATGT ATCAAACCTCA TCTCTCTATA TATATATATT CAATTGTTTT AAAAAAAAAA	1611
AAAAAAAAAA A	1622

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1605 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Petunia hybrida

(F) TISSUE TYPE: petal

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library

(B) CLONE: pPAT48

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 67..1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTCGACGAA ATCCATTTCA TTTCTCTTC TTTCTTGTTT TTCTAATTTC GTCATCATTG	60
TTATCC ATG GCA GGT GAA GTA GCA AAA CAA GAA GTT ACA AAA GTG AAA	108
Met Ala Gly Glu Val Ala Lys Gln Glu Val Thr Lys Val Lys	
1 5 10	
GTC CTG AAA AAA ACA AAC GTG AAA CCA CAT AAA CCA CTA GGA AAA AAA	156
Val Leu Lys Lys Thr Asn Val Lys Pro His Lys Pro Leu Gly Lys Lys	
15 20 25 30	
GAG TGT CAA TTG GTA ACA TTT GAT CTT CCT TAC CTA GCT TTC TAT TAC	204
Glu Cys Gln Leu Val Thr Phe Asp Leu Pro Tyr Leu Ala Phe Tyr Tyr	
35 40 45	
AAC CAA AAA TTT CTC ATC TAT AAA GGT GCT GAA AAC TTT GAC GAG ACG	252
Asn Gln Lys Phe Leu Ile Tyr Lys Gly Ala Glu Asn Phe Asp Glu Thr	
50 55 60	
GTG GAA AAA ATT AAA GAT GGA CTG GCC TTA GTA TTG GTG GAT TTC TAT	300
Val Glu Lys Ile Lys Asp Gly Leu Ala Leu Val Leu Val Asp Phe Tyr	
65 70 75	
CAA CTA GCT GGG AAA CTT GGA AAA GAT GAA GAA GGG GTT TTC AGG GTG	348
Gln Leu Ala Gly Lys Leu Gly Lys Asp Glu Glu Gly Val Phe Arg Val	
80 85 90	
GAA TAC GAC GAT GAC ATG GAT GGT GTA GAG GTG ACA GTG GCT GTT GCA	396
Glu Tyr Asp Asp Asp Met Asp Gly Val Glu Val Thr Val Ala Val Ala	
95 100 105 110	



GAA GAG ATA GAA GTT GCA GAT CTT ACT GAT GAA GAA GGC ACC ACC AAA Glu Glu Ile Glu Val Ala Asp Leu Thr Asp Glu Glu Gly Thr Thr Lys 115 120 125	444
TTG CAG GAC TTG ATT CCT TGT AAT AAA ATC TTG AAT TTG GAA GGG CTT Leu Gln Asp Leu Ile Pro Cys Asn Lys Ile Leu Asn Leu Glu Gly Leu 130 135 140	492
CAT CGC CCT CTT CTA GCT GTG CAG CTC ACC AAG CTC AAG GAC GGG CTC His Arg Pro Leu Leu Ala Val Gln Leu Thr Lys Leu Lys Asp Gly Leu 145 150 155	540
ACC ATG GGA TTA GCA TTT AAC CAT GCT GTG CTG GAT GGT ACT TCG ACG Thr Met Gly Leu Ala Phe Asn His Ala Val Leu Asp Gly Thr Ser Thr 160 165 170	588
TGG CAC TTT ATG ACC TCG TGG TCC GAG CTT TGC TGT GGG TCC ACC TCA Trp His Phe Met Thr Ser Trp Ser Glu Leu Cys Cys Gly Ser Thr Ser 175 180 185 190	636
ATT TCT GTC CCA CCA TTC CTT GAA CGA ACC AAG GCT CGT AAC ACT CGA Ile Ser Val Pro Pro Phe Leu Glu Arg Thr Lys Ala Arg Asn Thr Arg 195 200 205	684
GTC AAG CTC AAC CTC TCT CAA CCA TCA GAT GCA CCC GAA CAT GCT AAG Val Lys Leu Asn Leu Ser Gln Pro Ser Asp Ala Pro Glu His Ala Lys 210 215 220	732
TCA GCA ACC AAC GGT GAT GTC CCG GCC AAC GTA GAC CCA CCT CTT CGC Ser Ala Thr Asn Gly Asp Val Pro Ala Asn Val Asp Pro Pro Leu Arg 225 230 235	780
GAA AGA GTA TTC AAG TTC TCC GAG TTA GCA ATT GAC AAA ATC AAG TCA Glu Arg Val Phe Lys Phe Ser Glu Leu Ala Ile Asp Lys Ile Lys Ser 240 245 250	828
ACA GTC AAT GCC AAC TCA GGA GAG ACG CCA TTC TCC ACA TTC CAA TCA Thr Val Asn Ala Asn Ser Gly Glu Thr Pro Phe Ser Thr Phe Gln Ser 255 260 265 270	876
CTC TCC GCA CAC GTG TGG CTA GCC GTC ACA CGT GCG CGC CAA CTC AAG Leu Ser Ala His Val Trp Leu Ala Val Thr Arg Ala Arg Gln Leu Lys 275 280 285	924
CCC GAG GAC TAC ACT GTG TAC ACT GTG TTT GCT GAT TGC AGG AAA AGG Pro Glu Asp Tyr Thr Val Tyr Thr Val Phe Ala Asp Cys Arg Lys Arg 290 295 300	972
GTT GAT CCT CCA ATG CCA GAA AGT TAC TTC GGC AAC CTA ATT CAG GCA Val Asp Pro Pro Met Pro Glu Ser Tyr Phe Gly Asn Leu Ile Gln Ala 305 310 315	1020
ATT TTC ACA GTG ACC GCG GCA GGT TTG TTA CTA GCA AGC CCG ATC GAG Ile Phe Thr Val Thr Ala Ala Gly Leu Leu Leu Ala Ser Pro Ile Glu 320 325 330	1068

TTC GCT GGT GGG ATG ATA CAA CAA GCG ATC GTG AAG CAT GAC GCT AAG	1116
Phe Ala Gly Gly Met Ile Gln Gln Ala Ile Val Lys His Asp Ala Lys	
335 340 345 350	
GCC ATT GAT GAA AGA AAC AAG GAG TGG GAG AGC AAC CCG AAG ATC TTT	1164
Ala Ile Asp Glu Arg Asn Lys Glu Trp Glu Ser Asn Pro Lys Ile Phe	
355 360 365	
CAG TAC AAA GAT GCT GGA GTG AAC TGT GTT GCT GTT GGA AGT TCG CCA	1212
Gln Tyr Lys Asp Ala Gly Val Asn Cys Val Ala Val Gly Ser Ser Pro	
370 375 380	
AGG TTC AAG GTT TAC GAC GTG GAT TTT GGA TGG GGA AAG CCA GAG AGT	1260
Arg Phe Lys Val Tyr Asp Val Asp Phe Gly Trp Gly Lys Pro Glu Ser	
385 390 395	
GTG AGG AGT GGT TCG AAC AAT AGG TTT GAT GGA ATG GTG TAT TTG TAC	1308
Val Arg Ser Gly Ser Asn Asn Arg Phe Asp Gly Met Val Tyr Leu Tyr	
400 405 410	
CAA GGC AAA AAT GGA GGA AGA AGC ATT GAT GTG GAG ATT AGT TTG GAA	1356
Gln Gly Lys Asn Gly Gly Arg Ser Ile Asp Val Glu Ile Ser Leu Glu	
415 420 425 430	
GCA AAT GCT ATG GAG AGG TTG GAG AAA GAT AAA GAG TTC CTC ATG GAA	1404
Ala Asn Ala Met Glu Arg Leu Glu Lys Asp Lys Glu Phe Leu Met Glu	
435 440 445	
ACT GCT TAATTTGCTT AGCTTGGA CT CAACTGGCTA CACTTTATTT ATGAGCTGCT	1460
Thr Ala	
ATGACTCACA TGCATGTATG TTTATTTTTT TTGGAGGGGT TCTTTCCTTT TATTGTTTTT	1520
TATGTTTTTT CTTTCTTGTA CGTTATGAAG AGAAACCGAG TATAAAGGAA TAATGTTTTT	1580
AGTTATTAAA AAAAAAAAAA AAAAA	1605

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Perilla ocimoides*

(F) TISSUE TYPE: leaf

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library

(B) CLONE: pSAT208

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..1340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CC GTG ATC GAA ACG TGT AGA GTT GGG CCG CCG CCG GAC TCG GTG GCG	47
Val Ile Glu Thr Cys Arg Val Gly Pro Pro Pro Asp Ser Val Ala	
1 5 10 15	
GAG CAA TCG GTG CCG CTC ACA TTC TTC GAC ATG ACG TGG CTG CAT TTT	95
Glu Gln Ser Val Pro Leu Thr Phe Phe Asp Met Thr Trp Leu His Phe	
20 25 30	
CAT CCC ATG CTT CAG CTC CTC TTC TAC GAA TTC CCT TGT TCC AAG CAA	143
His Pro Met Leu Gln Leu Leu Phe Tyr Glu Phe Pro Cys Ser Lys Gln	
35 40 45	
CAT TTT TCA GAA TCC ATC GTT CCA AAA CTC AAA CAA TCT CTC TCT AAA	191
His Phe Ser Glu Ser Ile Val Pro Lys Leu Lys Gln Ser Leu Ser Lys	
50 55 60	
ACT CTC ATA CAC TTC TTC CCT CTC TCA TGC AAT TTA ATC TAC CCT TCA	239
Thr Leu Ile His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr Pro Ser	
65 70 75	
TCC CCG GAG AAA ATG CCG GAG TTT CGG TAT CTA TCC GGG GAC TCG GTT	287
Ser Pro Glu Lys Met Pro Glu Phe Arg Tyr Leu Ser Gly Asp Ser Val	
80 85 90 95	
TCT TTC ACC ATC GCA GAA TCT AGC GAC GAC TTC GAT GAT CTC GTC GGA	335
Ser Phe Thr Ile Ala Glu Ser Ser Asp Asp Phe Asp Asp Leu Val Gly	
100 105 110	
AAT CGT CCA GAA TCT CCC GTT AGG CTC TAC AAC TTT GTC CCT AAA TTG	383
Asn Arg Pro Glu Ser Pro Val Arg Leu Tyr Asn Phe Val Pro Lys Leu	
115 120 125	
CCG CCC ATT GTC GAA GAA TCC GAT AGA AAA CTC TTC CAA GTT TTC GCC	431
Pro Pro Ile Val Glu Glu Ser Asp Arg Lys Leu Phe Gln Val Phe Ala	
130 135 140	
GTG CAG GTG ACT CTT TTC CCA GGC CGA GGC GTC GGT ATT GGA ATA GCA	479
Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Gly Ile Gly Ile Ala	
145 150 155	
ACG CAT CAC ACC GTT AGC GAC GCC CCG TCG TTT CTC GCG TTT ATA ACG	527
Thr His His Thr Val Ser Asp Ala Pro Ser Phe Leu Ala Phe Ile Thr	

160					165					170					175	
GCT	TGG	TCT	TCA	ATG	AGC	AAA	CAC	ATT	GAA	AAT	GAA	GAT	GAA	GAT	GAA	575
Ala	Trp	Ser	Ser	Met	Ser	Lys	His	Ile	Glu	Asn	Glu	Asp	Glu	Asp	Glu	
				180					185					190		
GAA	TTT	AAA	TCT	TTG	CCA	GTT	TTC	GAT	AGA	TCC	GTC	ATA	AAA	TAT	CCG	623
Glu	Phe	Lys	Ser	Leu	Pro	Val	Phe	Asp	Arg	Ser	Val	Ile	Lys	Tyr	Pro	
			195					200					205			
ACG	AAA	TTT	GAC	TCC	ATT	TAT	TGG	AGA	AAC	GCG	CTA	AAA	TTT	CCT	TTG	671
Thr	Lys	Phe	Asp	Ser	Ile	Tyr	Trp	Arg	Asn	Ala	Leu	Lys	Phe	Pro	Leu	
			210				215					220				
CAA	TCT	CGT	CAT	CCC	TCA	TTA	CCG	ACG	GAC	CGC	ATT	CGA	ACC	ACG	TTC	719
Gln	Ser	Arg	His	Pro	Ser	Leu	Pro	Thr	Asp	Arg	Ile	Arg	Thr	Thr	Phe	
			225			230					235					
GTT	TTC	ACC	CAA	TCC	AAA	ATT	AAG	AAA	TTG	AAG	GGT	TGG	ATT	CAG	TCC	767
Val	Phe	Thr	Gln	Ser	Lys	Ile	Lys	Lys	Leu	Lys	Gly	Trp	Ile	Gln	Ser	
240					245				250					255		
AGA	GTT	CCA	AGT	TTA	GTC	CAT	CTC	TCA	TCT	TTT	GTA	GCG	ATT	GCA	GCT	815
Arg	Val	Pro	Ser	Leu	Val	His	Leu	Ser	Ser	Phe	Val	Ala	Ile	Ala	Ala	
				260					265					270		
TAT	ATG	TGG	GCT	GGC	ATA	ACG	AAA	TCA	TTC	ACA	GCA	GAT	GAA	GAC	CAA	863
Tyr	Met	Trp	Ala	Gly	Ile	Thr	Lys	Ser	Phe	Thr	Ala	Asp	Glu	Asp	Gln	
			275					280					285			
GAC	AAC	GAG	GAT	GCA	TTT	TTC	TTG	ATT	CCG	GTC	GAT	CTA	AGG	CCA	CGA	911
Asp	Asn	Glu	Asp	Ala	Phe	Phe	Leu	Ile	Pro	Val	Asp	Leu	Arg	Pro	Arg	
			290				295					300				
TTA	GAT	CCG	CCG	GTT	CCT	GAA	AAT	TAC	TTC	GGG	AAC	TGC	TTA	TCG	TAC	959
Leu	Asp	Pro	Pro	Val	Pro	Glu	Asn	Tyr	Phe	Gly	Asn	Cys	Leu	Ser	Tyr	
	305					310					315					
GCG	CTG	CCG	AGA	ATG	CGG	CGG	CGA	GAG	CTG	GTG	GGA	GAG	AAA	GGG	GTG	1007
Ala	Leu	Pro	Arg	Met	Arg	Arg	Arg	Glu	Leu	Val	Gly	Glu	Lys	Gly	Val	
320					325				330					335		
TTT	CTG	GCA	GCT	GAG	GTA	ATC	GCG	GCG	GAG	ATA	AAA	AAA	AGG	ATC	AAC	1055
Phe	Leu	Ala	Ala	Glu	Val	Ile	Ala	Ala	Glu	Ile	Lys	Lys	Arg	Ile	Asn	
				340					345				350			
GAC	AAG	AGA	ATA	TTA	GAA	ACG	GTG	GAG	AAA	TGG	TCG	CCG	GAG	ATT	CGT	1103
Asp	Lys	Arg	Ile	Leu	Glu	Thr	Val	Glu	Lys	Trp	Ser	Pro	Glu	Ile	Arg	
				355				360					365			
AAA	GCG	TTG	CAG	AAA	TCA	TAT	TTT	TCG	GTG	GCA	GGA	TCG	AGC	AAG	CTA	1151
Lys	Ala	Leu	Gln	Lys	Ser	Tyr	Phe	Ser	Val	Ala	Gly	Ser	Ser	Lys	Leu	
			370				375					380				

GAT CTT TAC GGT GCA GAT TTT GGA TGG GGG AAG GCG AGA AAG CAA GAA	1199
Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala Arg Lys Gln Glu	
385 390 395	
ATA TTG TCG ATT GAT GGG GAG AAA TAT GCA ATG ACG CTT TGT AAA GCC	1247
Ile Leu Ser Ile Asp Gly Glu Lys Tyr Ala Met Thr Leu Cys Lys Ala	
400 405 410 415	
AGG GAT TTC GAA GGA GGA TTG GAG GTT TGC TTG TCT TTG CCT AAG GAC	1295
Arg Asp Phe Glu Gly Gly Leu Glu Val Cys Leu Ser Leu Pro Lys Asp	
420 425 430	
AAA ATG GAT GCT TTT GCT GCT TAT TTT TCA CTG GGA ATT AAT GGT	1340
Lys Met Asp Ala Phe Ala Ala Tyr Phe Ser Leu Gly Ile Asn Gly	
435 440 445	
TAATAAATGT ATGTAATTAA ACTAATATTA TTATGTAACA ATTAATTAAG TGTTGAGTAA	1400
CGTGAAGAAT AATCCCTATT ATATATTTAT GATTTGGTTC AAATAAAGTG TAAAGCCTCT	1460
TGAAAAAAAA AAAAAAAAAA	1479

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1508 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Senecio cruentus*
  - (F) TISSUE TYPE: petal
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA library
  - (B) CLONE: pCAT8
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..1364
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TG AAC ATT CTC GAA CAT GCC CGA ATA TCG GCC CCC TCG GGC ACC ATC	47
Asn Ile Leu Glu His Ala Arg Ile Ser Ala Pro Ser Gly Thr Ile	
1 5 10 15	

GGC	CAT	CGC	TCG	TTA	TCT	CTT	ACT	TTC	TTC	GAC	ATT	ACT	TGG	CTA	CTC	95
Gly	His	Arg	Ser	Leu	Ser	Leu	Thr	Phe	Phe	Asp	Ile	Thr	Trp	Leu	Leu	
			20						25					30		
TTC	CCT	CCG	GTC	CAC	CAT	CTT	TTC	TTC	TAT	GAC	TTT	CCA	CAT	TCT	AAA	143
Phe	Pro	Pro	Val	His	His	Leu	Phe	Phe	Tyr	Asp	Phe	Pro	His	Ser	Lys	
			35					40				45				
TCC	CAT	TTC	ATG	GAC	ACT	ATT	GTT	CCC	AGG	CTA	AAA	CAA	TCT	TTA	TCG	191
Ser	His	Phe	Met	Asp	Thr	Ile	Val	Pro	Arg	Leu	Lys	Gln	Ser	Leu	Ser	
		50					55					60				
GTC	ACT	CTT	CAA	CAT	TTT	TTC	CCG	TTT	GCT	AGT	AAT	TTG	ATT	GTA	TTT	239
Val	Thr	Leu	Gln	His	Phe	Phe	Pro	Phe	Ala	Ser	Asn	Leu	Ile	Val	Phe	
	65					70					75					
CCT	AAC	ACT	GAT	GGT	TCG	GGT	TTT	AAT	AAA	AAA	CCA	GAA	ATA	AAA	CAC	287
Pro	Asn	Thr	Asp	Gly	Ser	Gly	Phe	Asn	Lys	Lys	Pro	Glu	Ile	Lys	His	
80					85					90					95	
GTT	GAA	GGT	GAT	TCT	GTT	GTG	GTT	ACT	TTT	GCA	GAA	TGT	TGT	CTT	GAC	335
Val	Glu	Gly	Asp	Ser	Val	Val	Val	Thr	Phe	Ala	Glu	Cys	Cys	Leu	Asp	
			100					105						110		
TTT	AAT	AAT	TTG	ACA	GGA	AAT	CAT	CCT	CGA	AAA	TGT	GAA	AAC	TTT	TAT	383
Phe	Asn	Asn	Leu	Thr	Gly	Asn	His	Pro	Arg	Lys	Cys	Glu	Asn	Phe	Tyr	
			115					120					125			
CCA	CTT	GTA	CCT	TCA	TTG	GGA	AAT	GCA	ATC	AAA	TTA	TGT	GAT	TGC	GTC	431
Pro	Leu	Val	Pro	Ser	Leu	Gly	Asn	Ala	Ile	Lys	Leu	Cys	Asp	Cys	Val	
		130					135					140				
ACG	GTC	CCA	CTT	TTT	TCA	CTT	CAA	GTG	ACG	TTT	TTT	CCG	GGC	TCG	GGT	479
Thr	Val	Pro	Leu	Phe	Ser	Leu	Gln	Val	Thr	Phe	Phe	Pro	Gly	Ser	Gly	
	145					150					155					
ATA	TCA	CTA	GGA	ATG	ACG	AAT	CAT	CAT	AGC	CTT	GGT	GAC	GCT	AGC	ACG	527
Ile	Ser	Leu	Gly	Met	Thr	Asn	His	His	Ser	Leu	Gly	Asp	Ala	Ser	Thr	
160					165				170						175	
CGG	TTC	AAC	TTT	TTG	AAA	GGG	TGG	ACT	TCG	ATT	ATT	CAA	TCT	GGT	GTA	575
Arg	Phe	Asn	Phe	Leu	Lys	Gly	Trp	Thr	Ser	Ile	Ile	Gln	Ser	Gly	Val	
			180					185					190			
GAT	CGG	TCT	TTT	TTA	ACG	AAA	GGA	TCT	CCA	CCG	GTT	TTT	GAT	AGA	TTG	623
Asp	Arg	Ser	Phe	Leu	Thr	Lys	Gly	Ser	Pro	Pro	Val	Phe	Asp	Arg	Leu	
			195					200					205			
ATT	AAC	ATC	CCA	CAT	TTA	GAT	GAA	AAT	AAG	TTG	AGA	CAT	ACA	AGG	CTC	671
Ile	Asn	Ile	Pro	His	Leu	Asp	Glu	Asn	Lys	Leu	Arg	His	Thr	Arg	Leu	
		210					215					220				
GAA	AGT	TTT	TAT	AAA	CCT	TCG	AGC	CTT	GTT	GGT	CCC	ACT	GAT	AAA	GTT	719
Glu	Ser	Phe	Tyr	Lys	Pro	Ser	Ser	Leu	Val	Gly	Pro	Thr	Asp	Lys	Val	
	225					230					235					

CGG TCA ACG TTT GTG TTG ACC CGA ACT AAT ATC AAT CTA CTA AAG AAA	767
Arg Ser Thr Phe Val Leu Thr Arg Thr Asn Ile Asn Leu Leu Lys Lys	
240 245 250 255	
AAG GTC TTA ACC CAA GTG CCA AAC TTG GAG TAC ATG TCA TCT TTT ACG	815
Lys Val Leu Thr Gln Val Pro Asn Leu Glu Tyr Met Ser Ser Phe Thr	
260 265 270	
GTA ACT TGT GGT TAT ATA TGG AGT TGC ATA GCG AAA TCA CTC GTA AAA	863
Val Thr Cys Gly Tyr Ile Trp Ser Cys Ile Ala Lys Ser Leu Val Lys	
275 280 285	
ATA GGA GAA AGA AAG GGC GAA GAC GAG TTA GAA CAG TTC ATA ATC ACC	911
Ile Gly Glu Arg Lys Gly Glu Asp Glu Leu Glu Gln Phe Ile Ile Thr	
290 295 300	
ATT GAT TGT CGA TCT CGT CTT GAT CCA CCA ATT CCC ACA GCC TAC TTT	959
Ile Asp Cys Arg Ser Arg Leu Asp Pro Pro Ile Pro Thr Ala Tyr Phe	
305 310 315	
GGT AAC TGT GGT GCA CCA TGT GTC CCG ACC TTA AAA AAT GTC GTT TTG	1007
Gly Asn Cys Gly Ala Pro Cys Val Pro Thr Leu Lys Asn Val Val Leu	
320 325 330 335	
ACT ACG GAA AAT GGG TAT GCA CTT GGT GCT AAA GTA ATT GGA GAG TCT	1055
Thr Thr Glu Asn Gly Tyr Ala Leu Gly Ala Lys Val Ile Gly Glu Ser	
340 345 350	
ATA TGC AAA ATG ATA TAT AAT AAG GAC GGA ATC TTG AAA GAT GCC GCG	1103
Ile Cys Lys Met Ile Tyr Asn Lys Asp Gly Ile Leu Lys Asp Ala Ala	
355 360 365	
AGA TGG CAT GAA CCT TTC ATG ATC CCG GCT AGG AAG ATT GGT GTT GCT	1151
Arg Trp His Glu Pro Phe Met Ile Pro Ala Arg Lys Ile Gly Val Ala	
370 375 380	
GGT ACA CCT AAG CTC AAC TTG TAC GAC TTT GAT TTT GGG TGG GGG AAG	1199
Gly Thr Pro Lys Leu Asn Leu Tyr Asp Phe Asp Phe Gly Trp Gly Lys	
385 390 395	
CGC ATA AAG TAT GAG ACT GTT TCA ATA GAC TAT AAT ACG TCG ATT TCT	1247
Arg Ile Lys Tyr Glu Thr Val Ser Ile Asp Tyr Asn Thr Ser Ile Ser	
400 405 410 415	
ATA AAT GCA AGC AAA ACA TCA GCA CAA GAT CTT GAA ATT GGA TTG AGT	1295
Ile Asn Ala Ser Lys Thr Ser Ala Gln Asp Leu Glu Ile Gly Leu Ser	
420 425 430	
CTA CCG AGT ATG CAA ATG GAG GCG TTT TCT AGC ATC TTT GAT GAA GGA	1343
Leu Pro Ser Met Gln Met Glu Ala Phe Ser Ser Ile Phe Asp Glu Gly	
435 440 445	
TTA GAG AGT CAA GTT TCA TTG TAGATCATCG TCCCCTTTTT GTGTGCATCA	1394
Leu Glu Ser Gln Val Ser Leu	
450	

AGTTTCTGTC GTTTTTATGA GTTGCCACTG TTCTATTCTT TAAGTATACC TTTCGACTAT 1454  
 GTTTTGAAGA TGCAACGATA TAAAATGAAA AAAAAAAAAA AAAAAAAAAA AAAA 1508

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lavandula angustifolia*
- (F) TISSUE TYPE: petal

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library
- (B) CLONE: pLAT21

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

NTG ACC ACC CTC CTC GAA TCC TCC CGA GTG GCG CCG CCT CCA GGC ACG	47
Xaa Thr Thr Leu Leu Glu Ser Ser Arg Val Ala Pro Pro Pro Gly Thr	
1 5 10 15	
GTG GCT GAG CAG TCA CTC CCG CTC ACC TTC TTC GAC ATG ACG TGG CTG	95
Val Ala Glu Gln Ser Leu Pro Leu Thr Phe Phe Asp Met Thr Trp Leu	
20 25 30	
CAT TTC CAC CCC ATG CTT CAG CTT CTC TTC TAC GAA CTC CCC TGT TCC	143
His Phe His Pro Met Leu Gln Leu Leu Phe Tyr Glu Leu Pro Cys Ser	
35 40 45	
AAA CCC GCC TTC CTC GAA ACC GTC GTT CCG AAA CTC AAA CAA TCC TTA	191
Lys Pro Ala Phe Leu Glu Thr Val Val Pro Lys Leu Lys Gln Ser Leu	
50 55 60	
TCT CTA ACC CTC AAA CAC TTC TTC CCC CTT TCA TGC AAT CTA ATC TAC	239
Ser Leu Thr Leu Lys His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr	
65 70 75 80	



CCT	CTA	TCG	CCG	GAG	AAA	ATG	CCG	GAG	TTC	CGG	TAT	CAG	AAC	GGT	GAC	287
Pro	Leu	Ser	Pro	Glu	Lys	Met	Pro	Glu	Phe	Arg	Tyr	Gln	Asn	Gly	Asp	
			85						90					95		
TCG	GTT	TCT	TTC	ACG	ATT	ATG	GAG	TCT	GTC	GGA	GAT	CAT	CCG	CAT	TCC	335
Ser	Val	Ser	Phe	Thr	Ile	Met	Glu	Ser	Val	Gly	Asp	His	Pro	His	Ser	
			100					105					110			
GCT	CAT	AAA	TAC	TAC	TGC	TTT	GCC	CCT	AGC	GAC	GAT	TAT	GAA	GAT	CTC	383
Ala	His	Lys	Tyr	Tyr	Cys	Phe	Ala	Pro	Ser	Asp	Asp	Tyr	Glu	Asp	Leu	
		115					120					125				
CAG	CTG	CCG	CCG	ATA	GTC	GAG	GAA	TCT	GAT	CGG	AAA	TTG	TTT	CAA	GTT	431
Gln	Leu	Pro	Pro	Ile	Val	Glu	Glu	Ser	Asp	Arg	Lys	Leu	Phe	Gln	Val	
	130					135					140					
TTA	GCC	GTG	CAA	GTG	ACT	CTG	TTT	CCC	GGT	CGC	GGG	GTG	TGC	ATC	GGA	479
Leu	Ala	Val	Gln	Val	Thr	Leu	Phe	Pro	Gly	Arg	Gly	Val	Cys	Ile	Gly	
145					150					155					160	
ATA	ACG	ACG	CAC	CAC	ACC	GTT	AGC	GAT	GCT	CCA	TCG	TTT	GTA	GGG	TTT	527
Ile	Thr	Thr	His	His	Thr	Val	Ser	Asp	Ala	Pro	Ser	Phe	Val	Gly	Phe	
			165					170						175		
ATG	AAG	AGT	TGG	GCT	TCC	ATC	ACT	AAA	TTC	GGA	GGA	GAT	GAT	GAA	TTC	575
Met	Lys	Ser	Trp	Ala	Ser	Ile	Thr	Lys	Phe	Gly	Gly	Asp	Asp	Glu	Phe	
			180					185					190			
TTG	GAC	GGA	AAA	GGT	GAA	TGT	TTG	CCG	GTT	TTC	GAC	CGA	TCG	CTC	GTG	623
Leu	Asp	Gly	Lys	Gly	Glu	Cys	Leu	Pro	Val	Phe	Asp	Arg	Ser	Leu	Val	
	195						200					205				
AAT	TAT	CCG	CCT	AAA	TTG	GAC	ACA	TAT	TTA	TGG	AAC	AAC	GCG	CAG	AAA	671
Asn	Tyr	Pro	Pro	Lys	Leu	Asp	Thr	Tyr	Leu	Trp	Asn	Asn	Ala	Gln	Lys	
	210					215					220					
CGT	CCG	TTG	GAA	TCG	CAG	CAT	CCA	TCT	TTA	CCG	ACG	GAT	CGG	ATT	CGA	719
Arg	Pro	Leu	Glu	Ser	Gln	His	Pro	Ser	Leu	Pro	Thr	Asp	Arg	Ile	Arg	
225					230					235					240	
GCT	ACC	TAC	CTT	TTC	ACC	CAA	TCT	GAA	ATT	AAG	AAA	TTG	AAG	GGT	TTG	767
Ala	Thr	Tyr	Leu	Phe	Thr	Gln	Ser	Glu	Ile	Lys	Lys	Leu	Lys	Gly	Leu	
			245						250					255		
ATT	CAG	AGA	AAA	GCC	CCA	AAT	GTA	GTT	AAT	CTC	TCT	TCC	TTC	GTC	GCG	815
Ile	Gln	Arg	Lys	Ala	Pro	Asn	Val	Val	Asn	Leu	Ser	Ser	Phe	Val	Ala	
			260					265					270			
ATC	GCA	GCT	TAT	ATC	TGG	ACC	GGC	ATC	GCC	AAA	TCG	GTC	GGA	GAT	TAC	863
Ile	Ala	Ala	Tyr	Ile	Trp	Thr	Gly	Ile	Ala	Lys	Ser	Val	Gly	Asp	Tyr	
		275					280					285				
AAA	GAC	GTG	GAT	GAC	GAC	AAA	CGC	GCT	TTC	TTT	TTA	ATT	CCG	ATC	GAT	911
Lys	Asp	Val	Asp	Asp	Asp	Lys	Arg	Ala	Phe	Phe	Leu	Ile	Pro	Ile	Asp	
	290					295					300					

TTA AGG CCG CGT TTG GAT CCG CCG GCT CCG GGG AAC TAC TTC GGA AAC	959
Leu Arg Pro Arg Leu Asp Pro Pro Ala Pro Gly Asn Tyr Phe Gly Asn	
305 310 315 320	
TGT CTA TCG TTT GCG ATG GCG AAG ATC CTG CGG CGG GAT TTG GTC GGA	1007
Cys Leu Ser Phe Ala Met Ala Lys Ile Leu Arg Arg Asp Leu Val Gly	
325 330 335	
GAT GAA GGG GTG TTT CGG GCA GCT GAG GCG ATC GCG GCG GAA ATA GAG	1055
Asp Glu Gly Val Phe Arg Ala Ala Glu Ala Ile Ala Ala Glu Ile Glu	
340 345 350	
AAG AGG ACG AGC GAC AAG AAG ATT CTA GAA ACT GTG GAG AAC TGG CCG	1103
Lys Arg Thr Ser Asp Lys Lys Ile Leu Glu Thr Val Glu Asn Trp Pro	
355 360 365	
TCT GAG ATT CGC GAA GCC TTG CAA AAC TGT TAT TTC TCG GTG GCG GGA	1151
Ser Glu Ile Arg Glu Ala Leu Gln Asn Cys Tyr Phe Ser Val Ala Gly	
370 375 380	
TCG AGC AGG CTT GAT CTT TAC GGC GCG GAT TTT GGA TGG GGT AAG GCG	1199
Ser Ser Arg Leu Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala	
385 390 395 400	
GTG AAG CAA GAG ATA CTG TCG ATT GAT GGA GAG AAG TTT ACG ATG TCG	1247
Val Lys Gln Glu Ile Leu Ser Ile Asp Gly Glu Lys Phe Thr Met Ser	
405 410 415	
TTG TGT AAA CCG AGG GAT GCT GCC GGA GGA TTG GAG GTT GGA TTG TCT	1295
Leu Cys Lys Pro Arg Asp Ala Ala Gly Gly Leu Glu Val Gly Leu Ser	
420 425 430	
TTG CCA AAG GAG GAA TTG CAA GCT TTT GAT GAT TAT TTT GCG GAG GGA	1343
Leu Pro Lys Glu Glu Leu Gln Ala Phe Asp Asp Tyr Phe Ala Glu Gly	
435 440 445	
ATA AAG GGT TGATTAATCA TTTAATCATG TATTATGAAG TTGGATGAAA	1392
Ile Lys Gly	
450	
TCCTCTGTTT CATCTCTATT GTTTAAACAA TAATTTTTTTT CCATTGAACT TTTTGTAGTC	1452
AATAAAAAAA AAAAAAAAATG AAAAAACTCA GTTATTTTTTT TTTTTTTTTT	1512
TTTTTTTTTT	1521

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg	Phe	Leu	Gly	Ile	Thr	Gly	Ser	Pro	Lys
1				5					10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ile	His	Met	Asp	Ala	Phe	Ala	Lys
1				5			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly	Val	Glu	Ile	Gly	Val	Ser	Leu	Pro	Lys
1				5					10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ser Leu Ser Leu Thr Leu Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Tyr Val Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val Arg Ala Thr Tyr Val Leu Ser Leu Ala Glu Ile Gln Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile His Met Asp Ala Phe Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Ile His Met Asp Ala Phe Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Ile His Met Asp Ala Phe Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AARATHCAYA TGGAYGCNTT YGC

23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTCGAGTTTT TTTTTTTTTT TTT

23

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCACCATGG AGCAAATCCA AATGGT

26

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGAGTCGCCC TCATCAC

17

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AACAGCTATG ACCATG

16

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Phe Gly Trp Gly Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAYTTYGGNT GGGGNAA

17

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGCAACTGT CTTGCGTCAT G

21

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATGTCAGG TGTGAGGTTT AAC

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCGTTTCGC ATGATTGAAC

20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCAGAAGAAC TCGTCAAGAA

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 12..53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGATCCAAC A ATG GAG CAA ATC CAA ATG GTG GCC GTG ATC GAA ACG TGT	50
Met Glu Gln Ile Gln Met Val Ala Val Ile Glu Thr Cys	
1 5 10	

AGA	
Arg	53

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTAAAACGAC GGCCAT

16

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGATCCAAC	A	ATG	GAG	CAA	ATC	CAA	ATG	GTG	AAC	ATT	CTC	GAA	C	45
	Met	Glu	Gln	Ile	Gln	Met	Val	Asn	Ile	Leu	Glu			
15						20						25		

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTCGGAGGAA TTCGGCACGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 18..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTCGGATCC AACAAATG ACC ACC CTC CTC GAA TCC  
Thr Thr Leu Leu Glu Ser  
15

35